

GenCore version 5.1.6.
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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:11:16 ; Search time 40 Seconds
(without alignments)
853.193 Million cell updates/sec

Title: US-09-922-895-1

Perfect score: 1854
Sequence: 1 MTSLSDFVEFGTSTSYDDY.....LERTSSVSPSTAPELSYF 355

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	99.8	355	2	G02436
2	1240	66.9	359	2	I49341
3	1181.5	63.7	355	2	A45177
4	1117.5	60.3	355	2	I49339
5	958.5	51.7	383	2	S55594
6	947	51.1	360	2	JC2443
7	938.5	50.6	352	2	A43113
8	927.5	50.0	356	2	I49340
9	886.5	47.8	374	2	I38450
10	803.5	43.3	360	2	A57160
11	780.5	42.1	360	2	JC587
12	710.5	38.3	354	2	I58186
13	692.5	37.4	355	2	JC5067
14	684	36.9	355	2	JC4304
15	659.5	35.6	344	2	JC5942
16	572	30.9	369	2	JC5068
17	541.5	29.2	378	2	B55735
18	527.5	28.5	378	2	A45680
19	524.5	28.3	367	2	JE0349
20	521	28.1	333	2	I65989
21	515	27.8	378	2	A55735
22	508	27.4	352	2	A45747
23	503	27.1	352	2	G00048
24	503	27.1	360	2	A53611
25	502	27.1	353	2	S28787
26	491.5	26.5	355	2	J01231
27	484.5	26.1	359	2	A42656
28	481.5	26.0	350	2	A39445
29	480.5	25.9	350	2	JN0621

30	478.5	25.8	358	2	A53752	Interleukin-8 rece
31	478	25.8	359	2	JC2134	angiotensin II rec
32	476	25.7	359	2	S44425	angiotensin II rec
33	474.5	25.6	359	2	J01516	angiotensin II rec
34	472	25.5	359	2	JH0621	angiotensin II rec
35	469	25.3	359	2	S15403	angiotensin II rec
36	466	25.1	362	2	JN0694	angiotensin II rec
37	465.5	25.1	359	2	JC1104	angiotensin II rec
38	465	25.1	359	2	A48857	angiotensin II rec
39	458.5	24.7	374	2	S42628	G protein-coupled
40	457.5	24.7	359	2	JC1194	angiotensin II rec
41	457	24.6	359	2	I51372	angiotensin II rec
42	454.5	24.5	359	2	I39418	angiotensin II rec
43	452.5	24.4	374	2	S32785	G protein-coupled
44	450	24.3	372	2	S2667	G protein-coupled
45	442.5	23.9	327	2	S56162	MCCR15 protein - h

ALIGNMENTS

RESULT 1

G02436

Chemokine (C-C) receptor 3 - human

N/Alternate names: C-C-CKR-3

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C/Accession: G02436; A57237

R/Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A/Reference number: H01272

A/Accession: G02436

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-355 <POND>

A/Cross-references: EMBL:U49727; NID:91477560; PIDN:AMB09726.1; PID:91477561

R/Combadlere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A/Title: Cloning and functional expression of a human eosinophil CC chemokine recepto

A/Reference number: A57237; MUID:95348056; PMID:7622448

A/Accession: A57237

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <CON>

A/Cross-references: GB:U28694; NID:91199579; PIDN:AAC50469.1; PID:91199580

A/Note: the translated sequence in GenBank entry HS028694, release 113.0, PIDN:AAC504

C/Genetics:

A/Gene: GDB:CKRBR3

A/Cross-references: GDB:579624; OMIM:601268

A/Map position: 3p21-3p21

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p

F:36-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-119/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-261/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:24-227, 106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte

Query Match 99.8%; Score 1851; DB 2; Length 355;
Best Local Similarity 99.7%; Pred. No. 1.1e-148;
Matches 354; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MTSLSDFVEFGTSTSYDDYGLCEKADTRALMAQFVPLSLVFTVGLGNVVVMI	60
Db	1	MTSLSDFVEFGTSTSYDDYGLCEKADTRALMAQFVPLSLVFTVGLGNVVVMI	60
Oy	61	KYRRLRIMTNLYLNLAIISDLFLVTLPEFWHYRGHNWPGHMCMLLSGFYTGXSE	120
Db	61	KYRRLRIMTNLYLNLAIISDLFLVTLPEFWHYRGHNWPGHMCMLLSGFYTGXSE	120

Db 197 -GMNETHIMNIGLVLPLLMVICYSIGILKTLIRCNKRHRRAVIFTIMIVLE 255
Oy 252 WTPYVALILSSYOSILEGNCDESKHDLVMTVEVIASHCCNPIYAFVGERFRY 311
Db 256 WTPYVALILMTFOEFGLSNCSQSOLDQATQVETIGIMHCCINPIIYAFVGERFRY 315
Oy 312 LRFHFHRLMLHMLGRTIFPLSEKIER-TSSVSPSTABEUS 352
Db 316 LSVFRRKHITRFKCKOCFVFEYFVGVSTWTFSTGEOEVS 357

RESULT 7
A3113
Chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CRF-5; CCR5
C:Species: Homo sapiens (man)
C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Ladbbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochembiol 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A:Reference number: S71808; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAML>
A:Cross-references: GB:U57840; NID:91502408; PIDN:CAA62796.1; PID:91262811
R:Samson, M.; Libert, F.; Doran, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imal, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles C
A:Reference number: S71808; MUID:96241590; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKRSHGAGPAAACGHLILGNPKNSASVK' <SAM3>
A:Cross-references: GB:X93393; NID:91524052; PIDN:CAA67767.1; PID:91524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a dege
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
J. leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CRF5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:91502408; PIDN:AA617071.1; PID:91502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', '91-352 <COM2>
A:Cross-references: EMBL:057840
R:Raport, C.J.; Gosling, J.; Schwickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:91457945; PIDN:AA605098.1; PID:91457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:J30574), MIP-1beta (see
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine
C:Genetics:
A:Gene: GDB:CMKR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21

C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RA
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: Vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmem
E:32-56/Domain: transmembrane #status predicted <TM1>
E:67-87/Domain: transmembrane #status predicted <TM2>
E:103-124/Domain: transmembrane #status predicted <TM3>
E:142-166/Domain: transmembrane #status predicted <TM4>
E:193-218/Domain: transmembrane #status predicted <TM5>
E:236-257/Domain: transmembrane #status predicted <TM6>
E:285-300/Domain: transmembrane #status predicted <TM7>
E:20-269/Domain: transmembrane #status predicted
E:268/Binding site: carbonyl bonds: #status predicted
E:336/337, 342/Binding site: phosphate (Ser) (covalent) #status predicted
E:340, 343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 50.6%; Score 927.5; DB 2; Length 352;
Best Local Similarity 50.7%; Pred. No. 8-71;
Matches 176; Conservative 68; Mismatches 102; Indels 1; Gaps 3;

Oy 24 CEKADTRALMAQVPEPLYSIVFTVGLGNVVVMTILIKYRLIMTNTILNLALISDLLE 83
Db 20 COKINVKQIAARLLPPLYSIVIFGFVGMVILLINKRKSTMDIYLLNLALISDLLE 79
Oy 84 LVTLPFWIHYRGHNVWFGHCKLLSGFYHTGLSEIFITLLTIDRYLAIVAAVFLR 143
Db 80 LITVPEWMAHYAA-OMDGNMTMCQLLTGLYIFGPFSGIIFITLLIDRYLAIVAAVFLR 138
Oy 144 ARTVFEVITSTVITGLVLAALPEIFETFELEETLSALYEDYVYSRHHHTRM 203
Db 139 ARTVFEVITSTVITGLVLAALPEIFETFELEETLSALYEDYVYSRHHHTRM 198
Oy 204 TIECLVPLVLAICYGTIGITLRLCPK-KKKYKARILFYMAVFEFTFVYVAAILLS 262
Db 199 VILGVLPVLAIVVVCISGILKTLRCRNEKKHRAVRLIFTMIYFLEFMAVYNVLLN 258
Oy 263 STQSLIFGDCRSKHLVMTVEVIASHCCNPIYAFVGERFRKTLRHFIRHLM 322
Db 259 TFOEFGGLNCCSSNRLOAMQVETLGTGTHCCINPIIYAFVGERFRNLLVFOKRIAK 318
Oy 323 HIGRTYIFLPSERKERTSSV-SPSTAEPLSTI 353
Db 319 RFCKCSITFOEAPERASSVYTRSTGEDEISV 350

RESULT 8
149340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: 149340
R:Guo, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chem
A:Reference number: 149339; MUID:95340546; PMID:7542241
A:Accession: 149340
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-356 <RES>
A:Cross-references: EMBL:028405; NID:9681549; PIDN:AA69154.1; PID:9681550
C:Superfamily: vertebrate rhodopsin

Query Match 50.0%; Score 927.5; DB 2; Length 356;
Best Local Similarity 50.7%; Pred. No. 8-71;
Matches 176; Conservative 68; Mismatches 102; Indels 1; Gaps 1;

Oy 7 TVEETGTSYDDV-GLICEKADTRALMAQVPEPLYSIVFTVGLGNVVVMTILIKYRL 65
Db 7 TSPSYTVAKNDFMGSGLCFPSINVRAFITVPTPLYSIVIFIGVGHVVLVLIQHRRL 66
Oy 66 RIMTNTIYLLNLALISDLLEPVTLPFWIHYRGHNVWFGHCKLLSGFYHTGLSEIFIT 125
Db 66 RIMTNTIYLLNLALISDLLEPVTLPFWIHYRGHNVWFGHCKLLSGFYHTGLSEIFIT 125

Db 67 RNNSTIYLFLNALISDLVFLSTLPEWVDYIMKGMIFGNACKFVSGFYVGLYDMFFIT 126
Qy 126 LITIDRYALVHAFALRARTVGTITSVTWGLAVLAALPEFIYETEELFEETLCSA 185
Db 127 LITIDRYALVHAFALRARTVGTITSVTWGLAVLAALPEFIYETEELFEETLCSA 186
Qy 186 LYEEDVYSNRHFTLMTIFCLVPLLVMAICTYGIITKLLRCPKSKKKAIRLIVIM 245
Db 187 ILPRKSLIRFLRCALTMNITLGLTLPPLAMICTYRIINVLHRRPNKKAKAVMLIFVIT 246
Qy 246 AVFEIEMTPYNAVAILLSSYSLFNGDCERSKHLDVMLVTEVAISGCCNPIYAFVG 305
Db 247 LLEFLLAPYLLAFVSAFEDVETPSCLSNQVDLSMTTEALATYHCCVNPVIVFVG 306
Qy 306 EERRKYLRFHFHRLHMLGRYIFLPELSEKLETSVSPSTAEPELS 352
Db 307 KRRFKYLMOLFRRHTAITLPQWLPFLSEDRAGASALPSTVEIETS 353

RESULT 9

138450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C-CCR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence, revision 16-Feb-1996 #text, change 13-Aug-1999
C:Accession: 138450
R:Chao, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins
A:Reference number: A53477; MUID:94195821; PMID:816186
A:Accession: 138450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:003882; NID:9472555; PIDN:AA19119.1; PID:9472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:134-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:33-277,113-190/Disulfide bonds: #status predicted

Query Match 47.8%; Score 886.5; DB 2; Length 374;
Best Local Similarity 54.2%; Pred. No. 2,66-67;
Matches 166; Conservative 57; Mismatches 72; Indels 11; Gaps 5;

Qy 14 TSYID-DVGLCEKADRALMAQFVPLYSLVFTVGLGNVVMILIKYRRLRIMNIX 72
Db 21 TTFEDYDYGAPCHRFVDVKQIGALPLPLYSLVFTFVGNNLVLLINCKKLCIDIX 80
Qy 73 LNLAIISDLFLVTLPLPMHIVRGHNWFGHGCKLLSGFHTGSLIFILLITDRY 132
Db 81 LNLAIISDLFLVTLPLMAHSA-ANENVFGNACKLFGTLGHISYFGGIFILLITDRY 139
Qy 133 LAIVHAFALRARTVGTITSVTWGLAVLAALPEFIYETEELFEETLCSALYEDTV 192
Db 140 LAIVHAFALRARTVGTITSVTWGLAVLAALPEFIYETEELFEETLCSALYEDTV 196
Qy 193 YSMRHFPLRMTIFCLVPLLVMAICTYGIITKLLRCPKSKKKAIRLIVIM 251
Db 197 -GMNFTIMRNIGLVPLIMVYSGILKTLRCNKKRHRNAVIVFTIMLVYLF 255
Qy 252 WTPFNVAAILSSYSLFNGDCERSKHLDVMLVTEVAISGCCNPIYAFVGERPKY 311

Db 256 WTPFNVAAILMTFOEFGLSNCSTISOLDQATOVETLGMTHCCINPIYAFVGERPKS- 314
Qy 312 LRHFFH 317
Db 315 ---LFH 317

RESULT 10

A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C-CCR-4
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence, revision 10-Nov-1995 #text, change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POK>
A:Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9711452
A>Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p

F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/Disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:189,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 43.3%; Score 803.5; DB 2; Length 360;
Best Local Similarity 46.2%; Pred. No. 2,56-60;
Matches 163; Conservative 68; Mismatches 113; Indels 9; Gaps 7;

Qy 3 TSLDVERFGTTSY-YDVGLCEKADRALMAQFVPLYSLVFTVGLGNVVMILIK 61
Db 9 TFLD--ESIVSNYLYESIPRCCKEKGKARGELPLPLYSLVFTVGLGNVVMILYLFK 66
Qy 62 YRLRIMNITLNLAIISDLFLVTLPLPMHIVRGHNWFGHGCKLLSGFHTGSLYSEI 121
Db 67 YRLRIMNITLNLAIISDLFLVTLPLPMHIVRGHNWFGHGCKLLSGFHTGSLYSEI 125
Qy 122 FEIILITDRYALVHAFALRARTVGTITSVTWGLAVLAALPEFIYETEELFEET 181
Db 126 FEVHMSIDRYALVHAFALRARTVGTITSVTWGLAVLAALPEFIYETEELFEET 185
Qy 182 LCSALYEDTVYSNRHFTLMTIFCLVPLLVMAICTYGIITKLLRCPKSKKKAIRLI 241
Db 186 YCKTYSINST-TWVLSLSEINILGLVPLIMVYSGILKTLRCNKKRHRNAVIM 244
Qy 242 FVIAVFEIEMTPYNAVAILLSSYSLFNGDCERSKHLDVMLVTEVAISGCCNPIY 301
Db 245 FAVVAVLFGFMTPIVIFLLEVLVELVLDCTFERRYIDVAIQATETLAFVHCCNPIY 304
Qy 302 AVGERPKYLRHFFH--RHLMLHGRYIFLPELSEKLEK--TSSVSPSTAEPEL 351
Db 305 FFLGKFRKYLQLFKTCRGLFV-TCYCGILLQIYSADTPSSSYQSTIMDHL 356

RESULT 11

